

Fig. 1

Human glycoprotein hormone β 10 polypeptide:

MKLAFLFLGPMALLLAGYGCVLGASSG¹NLR²TFVGCAVREF³FLAKPGCRGLR⁴ITTDACWGRCE⁵TWEKPILEPPYIEAHRVCTY⁶N⁷ETKQVTVKLENCAPGVDPFYTPVAIRCDGACSTATTECETI

Nucleic acid encoding human glycoprotein hormone β 10 polypeptide:

ATGAAGCTGGCATTCCTCTTCCCTTGCCCCCATGGCCCTCCTCCTCTGGC
TGGCTATGGCTGTGCTCCTCGGTGCCCTCCAGTGGGAACCTGCGCACCTTTG
TGGCTGTGCCGTGAGGAGTTTACTTTCCTGGCCAAAGAACCCAGGCTGC
AGGGCCCTTCGGATCACACGGATGCCCTGCTGGGTGCTGTGAGACCTG
GGAGAAACCCATTCTGGAACCCCTATATGAAGCCCATCATCGAGTCT
GTACCTAACAGAGACCAACAGGTGACTGTCAAGTGGCCCAACTGTGCC
CCGGAGTCGACCCCTTCTACACCTATCCGTGGCCATCCGCTGTGACTG
CGAGCCCTGCTCCACTGCCACCCACGGAGTGTGAGACCATCTGAGGCCGCT
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

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1879.

```

1 .....FCIPTEYTMHIERRECAAYCLTINTTICAGYCMTRDINGKL 40
      |   |:| .:| ||||| : :
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWE..KPI 47
89 FLPKYALSQD.VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCN 89
    || . |||| : ||.:| | |::.||||: |||||.
48 LEPPYIEAHHRVCTYNETHKQVTVKLPNCAPGVDPFYTFVAIRCDGACS 97
90 TDYSDCIHEAIKTNYCTKPQKSYLEVGFVS 118
    | .:| |||
98 TATTEC..ETI..... 106
```

Fig. 2B

GAP OF: HUMAN FSH- β CHECK: 8841 FROM: 1 TO: 111
 TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
 /GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
 COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	156	LENGTH:	122
RATIO:	1.472	GAPS:	3
PERCENT SIMILARITY:	44.211	PERCENT IDENTITY:	35.789

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
 | = IDENTITY
 : = 2
 . = 1

HUMAN FSH- β X HUMAN β 10

```

1 .....NSCELTNITIAIEKEEERFCISINTTWCAGYCYTRDL.VYK 40
      | . | . | | : | | | | | : : .
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVATQCHCGKCDSD 90
      | : ||: | ||: . | | | | | | . | | | .
50 PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDCGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
      .|:| |:
100 TTECETI..... 106
```

T0220"433T860

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GAP OF: HUMAN LH- β CHECK: 5679 FROM: 1 TO: 121

TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:

```

SYNOPSIS: COMPARE: INDEX:
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP

```

COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003

QUALITY:	140	LENGTH:	125
RATIO:	1.321	GAPS:	3
PERCENT SIMILARITY:	44.118	PERCENT IDENTITY:	32.353

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

```
| = IDENTITY
: = 2
. = 1
```

HUMAN LH- β X HUMAN β 10

```

1 .SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPTMMR.VLQ 46
   | | | | | | | | | | | | | | | | : : | | | | | | : : | :
1 ASSGNLRFTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

47 AVLPPLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRS 96
   | | | | : : .::| | | | | | | | .:| | |: | | | | .
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGCACSTA 99

97 TSDCGGPKDHPLTCDHPQLSGLLFL 121
   |.:|
100 TTECETI..... 106
```

Fig. 2D

GAP OF: HUMAN CG- β CHECK: 2358 FROM: 1 TO: 145
 TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
 /GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
 COMPHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	131	LENGTH:	149
RATIO:	1.236	GAPS:	3
PERCENT SIMILARITY:	42.157	PERCENT IDENTITY:	31.373

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
 | = IDENTITY
 : = 2
 . = 1

HUMAN CG- β X HUMAN β 10

```

1  .SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTR.VLQ 46
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEKPILE 49

47  GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPNVSYAVALSCQCALCRRS 96
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
50  PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDGACSTA 99

97  TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLSPSRLPGPSDTPILPQ 145
   |  |  |
100 TTECETI..... 106
  
```

FOAFOHSEB

Fig. 3

Fig. 3

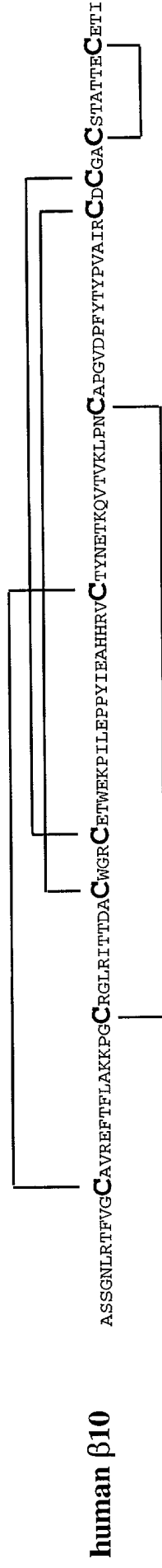


Fig. 4

BESTFIT of: human β 10 check: 6611 from: 1 to: 106

to: mouse β 10 check: 7740 from: 1 to: 106

Symbol comparison table: blosum62.cmp CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	577	Length:	106
Ratio:	5.443	Gaps:	0
Percent Similarity:	97.170	Percent Identity:	93.396

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

human β 10 x mouse β 10

```
1 ASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTDACWGRCEWKEKPILEP 50
. ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 SSSGNLHTFVGCAVREFTFMAKKPGCRGLRITTDACWGRCEWKEKPILEP 50

51 PYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTAT 100
||| |: ||||| |: ||||| ||||| ||||| ||||| ||||| |||||
51 PYIEAYHRVCTYNETRQVTVKLPNCAPGVDPFYTYPMAVRCDGACSTAT 100

101 TECETI 106
||| |||
101 TECETI 106
```

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